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WADA, Naoya
NAKAJIMA, Hiroto

<120> c-Jun phosphorylation inhibitor

<130> 3190-066

<140> US Unassigned

<141> 2004-09-27

<150> PCT/JP03/04120

<151> 2003-03-31

<150> JP P2002-095291

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<160> 90

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<210> 1

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<212> PRT

<213> Homo sapiens

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Gln Ser Leu Ser Ser Val Leu Gly Ser Gly Phe Gly Glu Leu Ala Pro
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Pro Lys Met Ala Asn Ile Thr Ser Ser Gln Ile Leu Asp Gln Leu Lys
35 40 45

Ala Pro Ser Leu Gly Gln Phe Thr Thr Thr Pro Ser Thr Gln Gln Asn
50 55 60

Ser Thr Ser His Pro Thr Thr Thr Thr Ser Trp Asp Leu Lys Pro Pro
65 70 75 80

Thr Ser Gln Ser Ser Val Leu Ser His Leu Asp Phe Lys Ser Gln Pro
 85 90 95

Glu Pro Ser Pro Val Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln
 100 105 110

Ser Gln Ala Val Thr Val Pro Pro Gly Leu Glu Ser Phe Pro Ser
 115 120 125

Gln Ala Lys Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val
 130 135 140

Asn Lys Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val
 145 150 155 160

Ser Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 165 170 175

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro Gly
 180 185 190

Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu Glu Phe
 195 200 205

Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro Ser Ser Glu
 210 215 220

Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys Ser Leu Ser Glu
 225 230 235 240

Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala Val Gln Asn Ser Thr
 245 250 255

Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser Leu Thr Ser Ser Ser Leu
 260 265 270

Asn Ser Ala Ser Pro Val Ala Met Ser Ser Ser Tyr Asp Gln Ser Ser
 275 280 285

Val His Asn Arg Ile Pro Tyr Gln Ser Pro Val Ser Ser Ser Glu Ser
 290 295 300

Ala Pro Gly Thr Ile Met Asn Gly His Gly Gly Gly Arg Ser Gln Gln
 305 310 315 320

Thr Leu Asp Thr Pro Lys Thr Thr Gly Pro Pro Ser Ala Leu Pro Ser
 325 330 335

Val Ser Ser Leu Pro Ser Thr Thr Ser Cys Thr Ala Leu Leu Pro Ser
 340 345 350

Thr Ser Gln His Thr Gly Asp Leu Thr Ser Ser Pro Leu Ser Gln Leu
 355 360 365

Ser Ser Ser Leu Ser Ser His Gln Ser Ser Leu Ser Ala His Ala Ala
 370 375 380

Leu Ser Ser Ser Thr Ser His Thr His Ala Ser Val Glu Ser Ala Ser
 385 390 395 400

Ser His Gln Ser Ser Ala Thr Phe Ser Thr Ala Ala Thr Ser Val Ser
 405 410 415

Ser Ser Ala Ser Ser Gly Val Ser Leu Ser Ser Ser Met Asn Thr Ala
 420 425 430

Asn Ser Leu Cys Leu Gly Gly Thr Pro Ala Ser Ala Ser Ser Ser Ser
 435 440 445

Ser Arg Ala Ala Pro Leu Val Thr Ser Gly Lys Ala Pro Pro Asn Leu
 450 455 460

Pro Gln Gly Val Pro Pro Leu Leu His Asn Gln Tyr Leu Val Gly Pro
 465 470 475 480

Gly Gly Leu Leu Pro Ala Tyr Pro Ile Tyr Gly Tyr Asp Glu Leu Gln
 485 490 495

Met Leu Gln Ser Arg Leu Pro Val Asp Tyr Tyr Gly Ile Pro Phe Ala
 500 505 510

Ala Pro Thr Ala Leu Ala Ser Arg Asp Arg Ser Leu Ala Asn Asn Pro
 515 520 525

Tyr Pro Gly Asp Val Thr Lys Phe Gly Arg Gly Asp Ser Ala Ser Pro
530 535 540

Ala Pro Ala Thr Thr Pro Ala Gln Pro Gln Gln Ser Gln Ser Gln Thr
545 550 555 560

His His Thr Ala Gln Gln Pro Phe Val Asn Pro Ala Leu Pro Pro Gly
565 570 575

Tyr Ser Tyr Thr Gly Leu Pro Tyr Tyr Thr Gly Met Pro Ser Ala Phe
580 585 590

Gln Tyr Gly Pro Thr Met Phe Val Pro Pro Ala Ser Ala Lys Gln His
595 600 605

Gly Val Asn Leu Ser Thr Pro Thr Pro Pro Phe Gln Gln Ala Ser Gly
610 615 620

Tyr Gly Gln His Gly Tyr Ser Thr Gly Tyr Asp Asp Leu Thr Gln Gly
625 630 635 640

Thr Ala Ala Gly Asp Tyr Ser Lys Gly Gly Tyr Ala Gly Ser Ser Gln
645 650 655

Ala Pro Asn Lys Ser Ala Gly Ser Gly Pro Gly Lys Gly Val Ser Val
660 665 670

Ser Ser Ser Thr Thr Gly Leu Pro Asp Met Thr Gly Ser Val Tyr Asn
675 680 685

Lys Thr Gln Thr Phe Asp Lys Gln Gly Phe His Ala Gly Thr Pro Pro
690 695 700

Pro Phe Ser Leu Pro Ser Val Leu Gly Ser Thr Gly Pro Leu Ala Ser
705 710 715 720

Gly Ala Ala Pro Gly Tyr Ala Pro Pro Pro Phe Leu His Ile Leu Pro
725 730 735

Ala His Gln Gln Pro His Ser Gln Leu Leu His His His Leu Pro Gln
740 745 750

Asp Ala Gln Ser Gly Ser Gly Gln Arg Ser Gln Pro Ser Ser Leu Gln
755 760 765

Pro Lys Ser Gln Ala Ser Lys Pro Ala Tyr Gly Asn Ser Pro Tyr Trp
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Thr Asn
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20 25 30

Asp Thr Ser Glu Phe Gln Val Gln Ala Pro Ala Arg Gly Thr Leu Gly
35 40 45

Arg Val Tyr Pro Gly Ser Arg Ser Ser Glu Lys His Ser Pro Asp Ser
50 55 60

Ala Cys Ser Val Asp Tyr Ser Ser Ser Cys Leu Ser Ser Pro Glu His
65 70 75 80

Pro Thr Glu Asp Ser Glu Ser Thr Glu Pro Leu Ser Val Asp Gly Ile
85 90 95

Ser Ser Asp Leu Glu Glu Pro Ala Glu Gly Asp Glu Glu Glu Glu Glu
100 105 110

Glu Glu Gly Gly Met Gly Pro Tyr Gly Leu Gln Glu Gly Ser Pro Gln
115 120 125

Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr Leu Ala
130 135 140

Ser Gly Ala Ala Pro Gly Ala Pro Val Gln Val Pro Glu Arg Ser Glu

145		150		155		160
Ser Arg Ser Ile	Ser Ser Arg Phe	Leu Leu Gln Val	Gln Thr Arg Pro			
	165		170		175	
Leu Arg Glu Pro	Ser Pro Ser Ser	Ser Ser Leu Ala	Leu Met Ser Arg			
	180		185		190	
Pro Ala Gln Val	Pro Gln Ala Ser	Gly Glu Gln Pro	Arg Gly Asn Gly			
	195		200		205	
Ala Asn Pro Pro	Gly Ala Pro Pro	Glu Val Glu Pro	Ser Ser Gly Asn			
	210		215		220	
Pro Ser Pro Gln	Gln Ala Ala Ser	Val Leu Leu Pro	Arg Cys Arg Leu			
	225		230		235	
Asn Pro Asp Ser	Ser Trp Ala Pro	Lys Arg Val Ala	Thr Ala Ser Pro			
	245		250		255	
Phe Ser Gly Leu	Gln Lys Ala Gln	Ser Val His Ser	Leu Val Pro Gln			
	260		265		270	
Glu Arg His Glu	Ala Ser Leu Gln	Ala Pro Ser Pro	Gly Ala Leu Leu			
	275		280		285	
Ser Arg Glu Ile	Glu Ala Gln Asp	Gly Leu Gly Ser	Leu Pro Pro Ala			
	290		295		300	
Asp Gly Pro Pro	Ser Arg Pro His	Ser Tyr Gln Asn	Pro Thr Thr Ser			
	305		310		315	
Ser Met Ala Lys	Ile Ser Arg Ser	Ile Ser Val Gly	Glu Asn Leu Gly			
	325		330		335	
Leu Val Ala Glu	Pro Gln Ala His	Ala Pro Ile Arg	Val Ser Pro Leu			
	340		345		350	
Ser Lys Leu Ala	Leu Pro Ser Arg	Ala His Leu Val	Leu Asp Ile Pro			
	355		360		365	
Lys Pro Leu Pro	Asp Arg Pro Thr	Leu Ala Ala Phe	Ser Pro Val Thr			

370

375

380

Lys Gly Arg Ala Pro Gly Glu Ala Glu Lys Pro Gly Phe Pro Val Gly
 385 390 395 400

Leu Gly Lys Ala His Ser Thr Thr Glu Arg Trp Ala Cys Leu Gly Glu
 405 410 415

Gly Thr Thr Pro Lys Pro Arg Thr Glu Cys Gln Ala His Pro Gly Pro
 420 425 430

Ser Ser Pro Cys Ala Gln Gln Leu Pro Val Ser Ser Leu Phe Gln Gly
 435 440 445

Pro Glu Asn Leu Gln Pro Pro Pro Pro Glu Lys Thr Pro Asn Pro Met
 450 455 460

Glu Cys Thr Lys Pro Gly Ala Ala Leu Ser Gln Asp Ser Ala Val Ser
 465 470 475 480

Leu Glu Gln Cys Glu Gln Leu Val Ala Glu Leu Arg Gly Ser Val Arg
 485 490 495

Gln Ala Val Arg Leu Tyr His Ser Val Ala Gly Cys Lys Met Pro Ser
 500 505 510

Ala Glu Gln Ser Arg Ile Ala Gln Leu Leu Arg Asp Thr Phe Ser Ser
 515 520 525

Val Arg Gln Glu Leu Glu Ala Val Ala Gly Ala Val Leu Ser Ser Pro
 530 535 540

Gly Ser Ser Pro Gly Ala Val Gly Ala Glu Gln Thr Gln Ala Leu Leu
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Glu Gln Tyr Ser Glu Leu Leu Leu Arg Ala Val Glu Arg Arg Met Glu
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Arg Lys Leu

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<211> 1217

<212> PRT
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<400> 3

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Cys Ser Tyr Phe Val Thr Ala Gly Asn Arg His Ile Lys Phe Trp Tyr
20 25 30

Leu Asp Asp Ser Lys Thr Ser Lys Val Asn Ala Thr Val Pro Leu Leu
35 40 45

Gly Arg Ser Gly Leu Leu Gly Glu Leu Arg Asn Asn Leu Phe Thr Asp
50 55 60

Val Ala Cys Gly Arg Gly Lys Lys Ala Asp Ser Thr Phe Cys Ile Thr
65 70 75 80

Ser Ser Gly Leu Leu Cys Glu Phe Ser Asp Arg Arg Leu Leu Asp Lys
85 90 95

Trp Val Glu Leu Arg Val Tyr Pro Glu Val Lys Asp Ser Asn Gln Ala
100 105 110

Cys Leu Pro Pro Ser Ser Phe Ile Thr Cys Ser Ser Asp Asn Thr Ile
115 120 125

Arg Leu Trp Asn Thr Glu Ser Ser Gly Val His Gly Ser Thr Leu His
130 135 140

Arg Asn Ile Leu Ser Ser Asp Leu Ile Lys Ile Ile Tyr Val Asp Gly
145 150 155 160

Asn Thr Gln Ala Leu Leu Asp Thr Glu Leu Pro Gly Gly Asp Lys Ala
165 170 175

Asp Ala Ser Leu Leu Asp Pro Arg Val Gly Ile Arg Ser Val Cys Val
180 185 190

Ser Pro Asn Gly Gln His Leu Ala Ser Gly Asp Arg Met Gly Thr Leu
195 200 205

Arg Val His Glu Leu Gln Ser Leu Ser Glu Met Leu Lys Val Glu Ala
 210 215 220

His Asp Ser Glu Ile Leu Cys Leu Glu Tyr Ser Lys Pro Asp Thr Gly
 225 230 235 240

Leu Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu Ile His Val Leu
 245 250 255

Asp Ala Gly Arg Glu Tyr Ser Leu Gln Gln Thr Leu Asp Glu His Ser
 260 265 270

Ser Ser Ile Thr Ala Val Lys Phe Ala Ala Ser Asp Gly Gln Val Arg
 275 280 285

Met Ile Ser Cys Gly Ala Asp Lys Ser Ile Tyr Phe Arg Thr Ala Gln
 290 295 300

Lys Ser Gly Asp Gly Val Gln Phe Thr Arg Thr His His Val Val Arg
 305 310 315 320

Lys Thr Thr Leu Tyr Asp Met Asp Val Glu Pro Ser Trp Lys Tyr Thr
 325 330 335

Ala Ile Gly Cys Gln Asp Arg Asn Ile Arg Ile Phe Asn Ile Ser Ser
 340 345 350

Gly Lys Gln Lys Lys Leu Phe Lys Gly Ser Gln Gly Glu Asp Gly Thr
 355 360 365

Leu Ile Lys Val Gln Thr Asp Pro Ser Gly Ile Tyr Ile Ala Thr Ser
 370 375 380

Cys Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser Ser Gly Glu Cys
 385 390 395 400

Val Ala Thr Met Phe Gly His Ser Glu Ile Val Thr Gly Met Lys Phe
 405 410 415

Ser Asn Asp Cys Lys His Leu Ile Ser Val Ser Gly Asp Ser Cys Ile
 420 425 430

Phe Val Trp Arg Leu Ser Ser Glu Met Thr Ile Ser Met Arg Gln Arg
435 440 445

Leu Ala Glu Leu Arg Gln Arg Gln Arg Gly Gly Lys Gln Gln Gly Pro
450 455 460

Ser Ser Pro Gln Arg Ala Ser Gly Pro Asn Arg His Gln Ala Pro Ser
465 470 475 480

Met Leu Ser Pro Gly Pro Ala Leu Ser Ser Asp Ser Asp Lys Glu Gly
485 490 495

Glu Asp Glu Gly Thr Glu Glu Glu Leu Pro Ala Leu Pro Val Leu Ala
500 505 510

Lys Ser Thr Lys Lys Ala Leu Ala Ser Val Pro Ser Pro Ala Leu Pro
515 520 525

Arg Ser Leu Ser His Trp Glu Met Ser Arg Ala Gln Glu Ser Val Gly
530 535 540

Phe Leu Asp Pro Ala Pro Ala Ala Asn Pro Gly Pro Arg Arg Arg Gly
545 550 555 560

Arg Trp Val Gln Pro Gly Val Glu Leu Ser Val Arg Ser Met Leu Asp
565 570 575

Leu Arg Gln Leu Glu Thr Leu Ala Pro Ser Leu Gln Asp Pro Ser Gln
580 585 590

Asp Ser Leu Ala Ile Ile Pro Ser Gly Pro Arg Lys His Gly Gln Glu
595 600 605

Ala Leu Glu Thr Ser Leu Thr Ser Gln Asn Glu Lys Pro Pro Arg Pro
610 615 620

Gln Ala Ser Gln Pro Cys Ser Tyr Pro His Ile Ile Arg Leu Leu Ser
625 630 635 640

Gln Glu Glu Gly Val Phe Ala Gln Asp Leu Glu Pro Ala Pro Ile Glu
645 650 655

Asp Gly Ile Val Tyr Pro Glu Pro Ser Asp Asn Pro Thr Met Asp Thr

660

665

670

Ser Glu Phe Gln Val Gln Ala Pro Ala Arg Gly Thr Leu Gly Arg Val
 675 680 685

Tyr Pro Gly Ser Arg Ser Ser Glu Lys His Ser Pro Asp Ser Ala Cys
 690 695 700

Ser Val Asp Tyr Ser Ser Ser Cys Leu Ser Ser Pro Glu His Pro Thr
 705 710 715 720

Glu Asp Ser Glu Ser Thr Glu Pro Leu Ser Val Asp Gly Ile Ser Ser
 725 730 735

Asp Leu Glu Glu Pro Ala Glu Gly Asp Glu Glu Glu Glu Glu Glu Glu
 740 745 750

Gly Gly Met Gly Pro Tyr Gly Leu Gln Glu Gly Ser Pro Gln Thr Pro
 755 760 765

Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr Leu Ala Ser Gly
 770 775 780

Ala Ala Pro Gly Ala Pro Val Gln Val Pro Glu Arg Ser Glu Ser Arg
 785 790 795 800

Ser Ile Ser Ser Arg Phe Leu Leu Gln Val Gln Thr Arg Pro Leu Arg
 805 810 815

Glu Pro Ser Pro Ser Ser Ser Ser Leu Ala Leu Met Ser Arg Pro Ala
 820 825 830

Gln Val Pro Gln Ala Ser Gly Glu Gln Pro Arg Gly Asn Gly Ala Asn
 835 840 845

Pro Pro Gly Ala Pro Pro Glu Val Glu Pro Ser Ser Gly Asn Pro Ser
 850 855 860

Pro Gln Gln Ala Ala Ser Val Leu Leu Pro Arg Cys Arg Leu Asn Pro
 865 870 875 880

Asp Ser Ser Trp Ala Pro Lys Arg Val Ala Thr Ala Ser Pro Phe Ser

885	890	895
Gly Leu Gln Lys Ala Gln Ser Val His Ser Leu Val Pro Gln Glu Arg		
900	905	910
His Glu Ala Ser Leu Gln Ala Pro Ser Pro Gly Ala Leu Leu Ser Arg		
915	920	925
Glu Ile Glu Ala Gln Asp Gly Leu Gly Ser Leu Pro Pro Ala Asp Gly		
930	935	940
Pro Pro Ser Arg Pro His Ser Tyr Gln Asn Pro Thr Thr Ser Ser Met		
945	950	955
Ala Lys Ile Ser Arg Ser Ile Ser Val Gly Glu Asn Leu Gly Leu Val		
965	970	975
Ala Glu Pro Gln Ala His Ala Pro Ile Arg Val Ser Pro Leu Ser Lys		
980	985	990
Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp Ile Pro Lys Pro		
995	1000	1005
Leu Pro Asp Arg Pro Thr Leu Ala Ala Phe Ser Pro Val Thr Lys		
1010	1015	1020
Gly Arg Ala Pro Gly Glu Ala Glu Lys Pro Gly Phe Pro Val Gly		
1025	1030	1035
Leu Gly Lys Ala His Ser Thr Thr Glu Arg Trp Ala Cys Leu Gly		
1040	1045	1050
Glu Gly Thr Thr Pro Lys Pro Arg Thr Glu Cys Gln Ala His Pro		
1055	1060	1065
Gly Pro Ser Ser Pro Cys Ala Gln Gln Leu Pro Val Ser Ser Leu		
1070	1075	1080
Phe Gln Gly Pro Glu Asn Leu Gln Pro Pro Pro Pro Glu Lys Thr		
1085	1090	1095
Pro Asn Pro Met Glu Cys Thr Lys Pro Gly Ala Ala Leu Ser Gln		

1100	1105	1110
Asp Ser Ala Val Ser Leu Glu Gln Cys Glu Gln Leu Val Ala Glu		
1115	1120	1125
Leu Arg Gly Ser Val Arg Gln Ala Val Arg Leu Tyr His Ser Val		
1130	1135	1140
Ala Gly Cys Lys Met Pro Ser Ala Glu Gln Ser Arg Ile Ala Gln		
1145	1150	1155
Leu Leu Arg Asp Thr Phe Ser Ser Val Arg Gln Glu Leu Glu Ala		
1160	1165	1170
Val Ala Gly Ala Val Leu Ser Ser Pro Gly Ser Ser Pro Gly Ala		
1175	1180	1185
Val Gly Ala Glu Gln Thr Gln Ala Leu Leu Glu Gln Tyr Ser Glu		
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Leu Leu Leu Arg Ala Val Glu Arg Arg Met Glu Arg Lys Leu		
1205	1210	1215
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Val Asp Cys Asn Arg Lys Arg Lys Gly Ser Ser Thr Asp Tyr Gln Glu		
	35	40 45
Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly Arg Leu Glu Tyr Thr		
	50	55 60
Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu Ala His Ser Gln Ile		
65	70	75 80

Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe Ile Asp Glu Leu Ala
85 90 95

Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg Lys Leu Asp Lys Leu
100 105 110

Thr Val Leu Arg Met Ala Val Gln His Met Lys Thr Leu Arg Gly Ala
115 120 125

Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro Thr Phe Leu Ser Asp
130 135 140

Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala Asp Gly Phe Leu Phe
145 150 155 160

Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe Val Ser Glu Ser Val
165 170 175

Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu Ile Gly Gln Ser Leu
180 185 190

Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys Val Lys Glu Gln Leu
195 200 205

Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu Ile Asp Ala Lys Thr
210 215 220

Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly Pro Ser Arg Leu Cys
225 230 235 240

Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met Lys Cys Asn Arg Pro
245 250 255

Ser Val Lys Val Glu Asp Lys Asp Phe Pro Ser Thr Cys Ser Lys Lys
260 265 270

Lys Ala Asp Arg Lys Ser Phe Cys Thr Ile His Ser Thr Gly Tyr Leu
275 280 285

Lys Ser Trp Pro Pro Thr Lys Met Gly Leu Asp Glu Asp Asn Glu Pro
290 295 300

Asp Asn Glu Gly Cys Asn Leu Ser Cys Leu Val Ala Ile Gly Arg Leu
 305 310 315 320

His Ser His Val Val Pro Gln Pro Val Asn Gly Glu Ile Arg Val Lys
 325 330 335

Ser Met Glu Tyr Val Ser Arg His Ala Ile Asp Gly Lys Phe Val Phe
 340 345 350

Val Asp Gln Arg Ala Thr Ala Ile Leu Ala Tyr Leu Pro Gln Glu Leu
 355 360 365

Leu Gly Thr Ser Cys Tyr Glu Tyr Phe His Gln Asp Asp Ile Gly His
 370 375 380

Leu Ala Glu Cys His Arg Gln Val Leu Gln Thr Arg Glu Lys Ile Thr
 385 390 395 400

Thr Asn Cys Tyr Lys Phe Lys Ile Lys Asp Gly Ser Phe Ile Thr Leu
 405 410 415

Arg Ser Arg Trp Phe Ser Phe Met Asn Pro Trp Thr Lys Glu Val Glu
 420 425 430

Tyr Ile Val Ser Thr Asn Thr Val Val Leu Ala Asn Val Leu Glu Gly
 435 440 445

Gly Asp Pro Thr Phe Pro Gln Leu Thr Ala Ser Pro His Ser Met Asp
 450 455 460

Ser Met Leu Pro Ser Gly Glu Gly Gly Pro Lys Arg Thr His Pro Thr
 465 470 475 480

Val Pro Gly Ile Pro Gly Gly Thr Arg Ala Gly Ala Gly Lys Ile Gly
 485 490 495

Arg Met Ile Ala Glu Glu Ile Met Glu Ile His Arg Ile Arg Gly Ser
 500 505 510

Ser Pro Ser Ser Cys Gly Ser Ser Pro Leu Asn Ile Thr Ser Thr Pro
 515 520 525

Pro Pro Asp Ala Ser Ser Pro Gly Gly Lys Lys Ile Leu Asn Gly Gly
 530 535 540

Thr Pro Asp Ile Pro Ser Ser Gly Leu Leu Ser Gly Gln Ala Gln Glu
 545 550 555 560

Asn Pro Gly Tyr Pro Tyr Ser Asp Ser Ser Ser Ile Leu Gly Glu Asn
 565 570 575

Pro His Ile Gly Ile Asp Met Ile Asp Asn Asp Gln Gly Ser Ser Ser
 580 585 590

Pro Ser Asn Asp Glu Ala Ala Met Ala Val Ile Met Ser Leu Leu Glu
 595 600 605

Ala Asp Ala Gly Leu Gly Gly Pro Val Asp Phe Ser Asp Leu Pro Trp
 610 615 620

Pro Leu
 625

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<400> 5

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Val Ser Asn Lys Gln Ala Gln Ile Leu Glu Pro Lys Pro Glu Pro Ser
 35 40 45

Leu Glu Ile Lys Pro Glu Gln Asp Gly Met Glu His Val Gly Arg Asp
 50 55 60

Asp Pro Lys Ala Leu Gly Glu Glu Pro Lys Gln Arg Arg Gly Ser Ala
 65 70 75 80

Ser Gly Ser Glu Pro Ala Gly Asp Ser Asp Arg Gly Gly Gly Pro Val
 85 90 95

Glu His Tyr His Leu His Leu Ser Ser Cys His Glu Cys Leu Glu Leu
 100 105 110

Glu Asn Ser Thr Ile Glu Ser Val Lys Phe Ala Ser Ala Glu Asn Ile
 115 120 125

Pro Asp Leu Pro Tyr Asp Tyr Ser Ser Ser Leu Glu Ser Val Ala Asp
 130 135 140

Glu Thr Ser Pro Glu Arg Glu Gly Arg Arg Val Asn Leu Thr Gly Lys
 145 150 155 160

Ala Pro Asn Ile Leu Leu Tyr Val Gly Ser Asp Ser Gln Glu Ala Leu
 165 170 175

Gly Arg Phe His Glu Val Arg Ser Val Leu Ala Asp Cys Val Asp Ile
 180 185 190

Asp Ser Tyr Ile Leu Tyr His Leu Leu Glu Asp Ser Ala Leu Arg Asp
 195 200 205

Pro Trp Thr Asp Asn Cys Leu Leu Leu Val Ile Ala Thr Arg Glu Ser
 210 215 220

Ile Pro Glu Asp Leu Tyr Gln Lys Phe Met Ala Tyr Leu Ser Gln Gly
 225 230 235 240

Gly Lys Val Leu Gly Leu Ser Ser Ser Phe Thr Phe Gly Gly Phe Gln
 245 250 255

Val Thr Ser Lys Gly Ala Leu His Lys Thr Val Gln Asn Leu Val Phe
 260 265 270

Ser Lys Ala Asp Gln Ser Glu Val Lys Leu Ser Val Leu Ser Ser Gly
 275 280 285

Cys Arg Tyr Gln Glu Gly Pro Val Arg Leu Ser Pro Gly Arg Leu Gln
 290 295 300

Gly His Leu Glu Asn Glu Asp Lys Asp Arg Met Ile Val His Val Pro

305		310		315		320
Phe Gly Thr Arg Gly Gly Glu Ala Val Leu Cys Gln Val His Leu Glu						
		325		330		335
Leu Pro Pro Ser Ser Asn Ile Val Gln Thr Pro Glu Asp Phe Asn Leu						
		340		345		350
Leu Lys Ser Ser Asn Phe Arg Arg Tyr Glu Val Leu Arg Glu Ile Leu						
		355		360		365
Thr Thr Leu Gly Leu Ser Cys Asp Met Lys Gln Val Pro Ala Leu Thr						
		370		375		380
Pro Leu Tyr Leu Leu Ser Ala Ala Glu Glu Ile Arg Asp Pro Leu Met						
		385		390		400
Gln Trp Leu Gly Lys His Val Asp Ser Glu Gly Glu Ile Lys Ser Gly						
		405		410		415
Gln Leu Ser Leu Arg Phe Val Ser Ser Tyr Val Ser Glu Val Glu Ile						
		420		425		430
Thr Pro Ser Cys Ile Pro Val Val Thr Asn Met Glu Ala Phe Ser Ser						
		435		440		445
Glu His Phe Asn Leu Glu Ile Tyr Arg Gln Asn Leu Gln Thr Lys Gln						
		450		455		460
Leu Gly Lys Val Ile Leu Phe Ala Glu Val Thr Pro Thr Thr Met Arg						
		465		470		475
Leu Leu Asp Gly Leu Met Phe Gln Thr Pro Gln Glu Met Gly Leu Ile						
		485		490		495
Val Ile Ala Ala Arg Gln Thr Glu Gly Lys Gly Arg Gly Gly Asn Val						
		500		505		510
Trp Leu Ser Pro Val Gly Cys Ala Leu Ser Thr Leu Leu Ile Ser Ile						
		515		520		525
Pro Leu Arg Ser Gln Leu Gly Gln Arg Ile Pro Phe Val Gln His Leu						

530

535

540

Met Ser Val Ala Val Val Glu Ala Val Arg Ser Ile Pro Glu Tyr Gln
 545 550 555 560

Asp Ile Asn Leu Arg Val Lys Trp Pro Asn Asp Ile Tyr Tyr Ser Asp
 565 570 575

Leu Met Lys Ile Gly Gly Val Leu Val Asn Ser Thr Leu Met Gly Glu
 580 585 590

Thr Phe Tyr Ile Leu Ile Gly Cys Gly Phe Asn Val Thr Asn Ser Asn
 595 600 605

Pro Thr Ile Cys Ile Asn Asp Leu Ile Thr Glu Tyr Asn Lys Gln His
 610 615 620

Lys Ala Glu Leu Lys Pro Leu Arg Ala Asp Tyr Leu Ile Ala Arg Val
 625 630 635 640

Val Thr Val Leu Glu Lys Leu Ile Lys Glu Phe Gln Asp Lys Gly Pro
 645 650 655

Asn Ser Val Leu Pro Leu Tyr Tyr Arg Tyr Trp Val His Ser Gly Gln
 660 665 670

Gln Val His Leu Gly Ser Ala Glu Gly Pro Lys Val Ser Ile Val Gly
 675 680 685

Leu Asp Asp Ser Gly Phe Leu Gln Val His Gln Glu Gly Gly Glu Val
 690 695 700

Val Thr Val His Pro Asp Gly Asn Ser Phe Asp Met Leu Arg Asn Leu
 705 710 715 720

Ile Leu Pro Lys Arg Arg
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 Gln Gln Asn Ser Thr Ser His Pro Thr Thr Thr Thr Ser Trp Asp Leu
 35 40 45
 Lys Pro Pro Thr Ser Gln Ser Ser Val Leu Ser His Leu Asp Phe Lys
 50 55 60
 Ser Gln Pro Glu Pro Ser Pro Val Leu Ser Gln Leu Ser Gln Arg Gln
 65 70 75 80
 Gln His Gln Ser Gln Ala Val Thr Val Pro Pro Pro Gly Leu Glu Ser
 85 90 95
 Phe Pro Ser Gln Ala Lys Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro
 100 105 110
 Ser Thr Val Asn Lys Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn
 115 120 125
 Ile Ser Val Ser Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala
 130 135 140
 Lys Arg Arg Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu
 145 150 155 160
 Met Pro Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala
 165 170 175
 Leu Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 180 185 190
 Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys Ser
 195 200 205
 Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala Val Gln
 210 215 220

Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser Leu Thr Ser
 225 230 235 240

Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser Ser Ser Tyr Asp
 245 250 255

Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln Ser Pro Val Ser Ser
 260 265 270

Ser Glu Ser Ala Pro Gly Thr Ile Met Asn Gly His Gly Gly Gly Arg
 275 280 285

Ser Gln Gln Thr Leu Asp Thr Pro Lys Thr Thr Gly Pro Pro Ser Ala
 290 295 300

Leu Pro Ser Val Ser Ser Leu Pro Ser Thr Thr Ser Cys Thr Ala Leu
 305 310 315 320

Leu Pro Ser Thr Ser Gln His Thr Gly Asp Leu Thr Ser Ser Pro Leu
 325 330 335

Ser Gln Leu Ser Ser Ser Leu Ser Ser His Gln Ser Ser Leu Ser Ala
 340 345 350

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Asn Thr Ala Asn Ser Leu Cys Leu Gly Gly Thr Pro Ala Ser Ala Ser
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Pro Asn Leu Pro Gln Gly Val Pro Pro Leu Leu His Asn Gln Tyr Leu
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Val Gly Pro Gly Gly Leu Leu Pro Ala Tyr Pro Ile Tyr Gly Tyr Asp
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Glu Leu Gln Met Leu Gln Ser Arg Leu Pro Val Asp Tyr Tyr Gly Ile
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Pro Phe Ala Ala Pro Thr Ala Leu Ala Ser Arg Asp Gly Ser Leu Ala
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Asn Asn Pro Tyr Pro Gly Asp Val Thr Lys Phe Gly Arg Gly Asp Ser
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Pro Pro Gly Tyr Ser Tyr Thr Gly Leu Pro Tyr Tyr Thr Gly Met Pro
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Ser Ala Phe Gln Tyr Gly Pro Thr Met Phe Val Pro Pro Ala Ser Ala
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Lys Gln His Gly Val Asn Leu Ser Thr Pro Thr Pro Pro Phe Gln Gln
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Ala Ser Gly Tyr Gly Gln His Gly Tyr Ser Thr Gly Tyr Asp Asp Leu
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Thr Gln Gly Thr Ala Ala Gly Asp Tyr Ser Lys Gly Gly Tyr Ala Gly
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Ser Ser Gln Ala Pro Asn Lys Ser Ala Gly Ser Gly Pro Gly Lys Gly
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Leu Ala Ser Gly Ala Ala Pro Gly Tyr Ala Pro Pro Phe Leu His
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<210> 12
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<212> PRT

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<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> a partial peptide of BPL1, which shows high homology with the peptide of SEQ ID NO:12

<400> 19

Leu Pro Pro Ser Ser Asn
1 5

<210> 20
 <211> 6
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> a partial peptide of BPL1, which shows high homology with the peptide of SEQ ID NO:13

<400> 20

Ala Val Leu Cys Gln Val
 1 5

<210> 21
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 21

Gln Pro Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro
 1 5 10 15

Pro Ser Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr
 20 25 30

Leu

<210> 22
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score in the local alignment between JNK3 and KIAA1491

<400> 22

Gln Ser Ser Ala Thr Phe Ser Thr Ala Ala Thr Ser Val Ser Ser Ser

1 5 10 15

Ala Ser Ser Gly Val Ser Leu Ser Ser Ser Met Asn Thr Ala Asn Ser
 20 25 30

Leu

<210> 23
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA1491 (SEQ ID NO:6)

<400> 23

Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser
 1 5 10 15

Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala
 20 25 30

Ser Asp Thr Asp Ser Ser Leu Glu Ala Ser Ala
 35 40

<210> 24
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of KIAA1491 (SEQ ID NO:6) showing high score in the local alignment between JNK3 and KIAA1491

<400> 24

Ala Ala Thr Ser Val Ser Ser Ser Ala Ser Ser Gly Val Ser Leu Ser
 1 5 10 15

Ser Ser Met Asn Thr Ala Asn Ser Leu Cys Leu Gly Gly Thr Pro Ala
 20 25 30

Ser Ala Ser Ser Ser Ser Ser Arg Ala Ala Pro
35 40

<210> 25
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and KIAA1491(
SEQ ID NO:6)

<400> 25

Phe Asp Lys Gln
1

<210> 26
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local align
ment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 26

His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn
1 5 10

<210> 27
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score
in the local alignment between JNK3 and KIAA1491

<400> 27

His Pro Thr Thr Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr
1 5 10

<210> 28
<211> 4

<212> PRT
 <213> Homo sapiens
 <220>
 <221> MISC_FEATURE
 <223> Partial sequence identical in the sequences of JNK3 and KIAA1491(
 SEQ ID NO:6)

<400> 28

Asp Leu Lys Pro
 1

<210> 29
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local align-
 ment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 29

Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser
 1 5 10 15

Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu
 20 25 30

<210> 30
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score
 in the local alignment between JNK3 and KIAA1491

<400> 30

Pro Tyr Gln Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile
 1 5 10 15

Met Asn Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu
 20 25

<210> 31
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and KIAA1491(
SEQ ID NO:6)

<400> 31

Ser Ser Glu Ser
1

<210> 32
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local align-
ment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 32

Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
1 5 10 15

Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp
20 25 30

Thr

<210> 33
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score
in the local alignment between JNK3 and KIAA1491

<400> 33

Thr Gly Asp Leu Thr Ser Ser Pro Leu Ser Gln Leu Ser Ser Ser Leu
1 5 10 15

Ser Ser His Gln Ser Ser Leu Ser Ala His Ala Ala Leu Ser Ser Ser
 20 25 30

Thr

<210> 34
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA1491 (SEQ ID NO:6)

<400> 34

Pro Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro
 1 5 10 15

Ser Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu
 20 25 30

Ala Ser Asp Thr Asp Ser Ser Leu Glu Ala Ser Ala
 35 40

<210> 35
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of KIAA1491 (SEQ ID NO:6) showing high score in the local alignment between JNK3 and KIAA1491

<400> 35

Ser Ser Pro Leu Ser Gln Leu Ser Ser Ser Leu Ser Ser His Gln Ser
 1 5 10 15

Ser Leu Ser Ala His Ala Ala Leu Ser Ser Ser Thr Ser His Thr His
 20 25 30

Ala Ser Val Glu Ser Ala Ser Ser His Gln Ser Ser Ala
 35 40 45

<210> 36
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 36

Gln Pro Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro
 1 5 10 15

Pro Ser Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln
 20 25 30

<210> 37
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 37

Gln Pro Pro Pro Pro Glu Lys Thr Pro Asn Pro Met Glu Cys Thr Lys
 1 5 10 15

Pro Gly Ala Ala Leu Ser Gln Asp Ser Ala Val Ser Leu Glu Gln
 20 25 30

<210> 38
 <211> 9
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 38

Phe Thr Pro Gln Lys Thr Leu Glu Glu
1 5

<210> 39

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score
in the local alignment between JNK3 and KIAA0596

<400> 39

Tyr Ser Leu Gln Gln Thr Leu Asp Glu
1 5

<210> 40

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of JNK3 showing high score in the local alignment
between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 40

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala
1 5 10 15

Gly Thr Ser Phe
20

<210> 41

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score
in the local alignment between JNK3 and KIAA0596

<400> 41

Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser Ser Gly Glu Cys Val
 1 5 10 15

Ala Thr Met Phe
 20

<210> 42
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 42

Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu
 1 5 10 15

<210> 43
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 43

Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu Ile His Val Leu
 1 5 10 15

<210> 44
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 44

Ser Leu Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln

1 5 10 15

Ala Arg Asp Leu Leu Ser Lys
20

<210> 45
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score
in the local alignment between JNK3 and KIAA0596

<400> 45

Ser Leu Val Pro Gln Glu Arg His Glu Ala Ser Leu Gln Ala Pro Ser
1 5 10 15

Pro Gly Ala Leu Leu Ser Arg
20

<210> 46
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alignment
between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 46

Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn Ser Glu
1 5 10 15

Glu

<210> 47
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 47

Leu Asp Lys Trp Val Glu Leu Arg Val Tyr Pro Glu Val Lys Asp Ser
1 5 10 15

Asn Gln

<210> 48

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 48

Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp Thr Asp
1 5 10

<210> 49

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 49

Ser Met Leu Ser Pro Gly Pro Ala Leu Ser Ser Asp Ser Asp
1 5 10

<210> 50

<211> 23

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 50

Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val Glu Val Gly Asp
1 5 10 15

Ser Thr Phe Thr Val Leu Lys
20

<210> 51

<211> 23

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 51

Thr Arg Glu Lys Ile Thr Thr Asn Cys Tyr Lys Phe Lys Ile Lys Asp
1 5 10 15

Gly Ser Phe Ile Thr Leu Arg
20

<210> 52

<211> 14

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 52

Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn
1 5 10

<210> 53

<211> 14

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 53

Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn
1 5 10

<210> 54

<211> 10

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 54

Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe
1 5 10

<210> 55

<211> 10

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 55

Glu Leu Leu Gly Thr Ser Cys Tyr Glu Tyr
1 5 10

<210> 56

<211> 22

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 56

Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp Thr Asp Ser Ser
 1 5 10 15

Leu Glu Ala Ser Ala Gly
 20

<210> 57
 <211> 22
 <212> PRT
 <213> homo sapiens
 <220>
 <221> misc_feature
 <223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 57

Ser Ser Pro Ser Asn Asp Glu Ala Ala Met Ala Val Ile Met Ser Leu
 1 5 10 15

Leu Glu Ala Asp Ala Gly
 20

<210> 58
 <211> 10
 <212> PRT
 <213> homo sapiens
 <220>
 <221> misc_feature
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 58

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe
 1 5 10

<210> 59
 <211> 10
 <212> PRT
 <213> homo sapiens
 <220>
 <221> misc_feature
 <223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 59

Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr
1 5 10

<210> 60

<211> 10

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 60

Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu
1 5 10

<210> 61

<211> 10

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 61

Phe Met Asn Pro Trp Thr Lys Glu Val Glu
1 5 10

<210> 62

<211> 11

<212> PRT

<213> homo sapiens

<220>

<221> misc_feature

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 62

Val Lys Gly Gln Pro Ser Pro Ser Gly Ala Ala
1 5 10

<210> 63
 <211> 11
 <212> PRT
 <213> homo sapiens

<220>
 <221> misc_feature
 <223> Partial oligopeptide of BMAL1 showing high score in the local alignment between JNK3 and BMAL1

<400> 63

Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala
 1 5 10

<210> 64
 <211> 31
 <212> PRT
 <213> homo sapiens

<220>
 <221> misc_feature
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL2

<400> 64

Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro Ser
 1 5 10 15

Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
 20 25 30

<210> 65
 <211> 31
 <212> PRT
 <213> homo sapiens

<220>
 <221> misc_feature
 <223> Partial oligopeptide of BMAL2 showing high score in the local alignment between JNK3 and BMAL2

<400> 65

Asp Asp Ser Ser Pro Thr Gly Leu Met Lys Asp Thr His Thr Val Asn
 1 5 10 15

Cys Arg Ser Met Ser Asn Lys Glu Leu Phe Pro Pro Ser Pro Ser
 20 25 30

<210> 66
 <211> 10
 <212> PRT
 <213> homo sapiens

<220>
 <221> misc_feature
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL2

<400> 66

Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe
 1 5 10

<210> 67
 <211> 10
 <212> PRT
 <213> homo sapiens

<220>
 <221> misc_feature
 <223> Partial oligopeptide of BMAL2 showing high score in the local alignment between JNK3 and BMAL2

<400> 67

Glu Leu Leu Gly Thr Ser Cys Tyr Glu Tyr
 1 5 10

<210> 68
 <211> 23
 <212> PRT
 <213> homo sapiens

<220>
 <221> misc_feature
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL2

<400> 68

Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val Glu Val Gly Asp
 1 5 10 15

Ser Thr Phe Thr Val Leu Lys
 20

<210> 69
<211> 23
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL2 showing high score in the local alignment between JNK3 and BMAL2

<400> 69

Ser Lys Glu Lys Ile Leu Thr Asp Ser Tyr Lys Phe Arg Ala Lys Asp
1 5 10 15

Gly Ser Phe Val Thr Leu Lys
20

<210> 70
<211> 12
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL2

<400> 70

Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val
1 5 10

<210> 71
<211> 12
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL2 showing high score in the local alignment between JNK3 and BMAL2

<400> 71

Ser Lys Lys Lys Glu His Arg Lys Phe Tyr Thr Ile
1 5 10

<210> 72
 <211> 8
 <212> PRT
 <213> homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 72

 Ser Tyr Leu Leu Tyr Gln Met Leu
 1 5

<210> 73
 <211> 8
 <212> PRT
 <213> homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 73

 Ser Tyr Ile Leu Tyr His Leu Leu
 1 5

<210> 74
 <211> 8
 <212> PRT
 <213> homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 74

 Ser Glu Pro Thr Leu Asp Val Lys
 1 5

<210> 75
 <211> 8
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 75

Pro Glu Pro Ser Leu Glu Ile Lys
 1 5

<210> 76
 <211> 14
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 76

Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys Ser
 1 5 10

<210> 77
 <211> 14
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 77

Val His Leu Glu Leu Pro Pro Ser Ser Asn Ile Val Gln Thr
 1 5 10

<210> 78
 <211> 9
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 78

Gln Lys Thr Leu Glu Glu Phe Gln Asp
1 5

<210> 79

<211> 9

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 79

Glu Lys Leu Ile Lys Glu Phe Gln Asp
1 5

<210> 80

<211> 4

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial sequence identical in the sequences of JNK3 and BPL1

<400> 80

Glu Phe Gln Asp
1

<210> 81

<211> 12

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 81

Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu
1 5 10

<210> 82
 <211> 11
 <212> PRT
 <213> homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 82

 Glu Ala Val Leu Cys Gln Val His Leu Glu Leu
 1 5 10

<210> 83
 <211> 4
 <212> PRT
 <213> homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> Partial sequence identical in the sequences of JNK3 and BPL1

<400> 83

 Leu Cys Gln Val
 1

<210> 84
 <211> 7
 <212> PRT
 <213> homo sapiens

 <220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 84

 Leu Pro Pro Ser Ser Ser Val
 1 5

<210> 85
 <211> 7
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 85

Leu Pro Pro Ser Ser Asn Ile
 1 5

<210> 86
 <211> 5
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial sequence identical in the sequences of JNK3 and BPL1

<400> 86

Leu Pro Pro Ser Ser
 1 5

<210> 87
 <211> 15
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 87

Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met
 1 5 10 15

<210> 88
 <211> 15
 <212> PRT
 <213> homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 88

Ser Gln Glu Ala Leu Gly Arg Phe His Glu Val Arg Ser Val Leu
1 5 10 15

<210> 89

<211> 11

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BPL1

<400> 89

Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu
1 5 10

<210> 90

<211> 11

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial oligopeptide of BPL1 showing high score in the local alignment between JNK3 and BPL1

<400> 90

Arg Ser Ile Pro Glu Tyr Gln Asp Ile Asn Leu
1 5 10

1